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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

THE APPLICATION OF:
STEPHEN M. ALLEN

CASE NO.: BB1429 US NA

APPLICATION NO.: 09/740,288

GROUP ART UNIT: UNKNOWN

FILED: CONCURRENTLY HEREWITH

EXAMINER: UNKNOWN

FOR: **PLANT BIOTIN SYNTHASE**

Assistant Commissioner for Patents
Washington, DC 20231

Sir:

DECLARATION IN ACCORDANCE WITH 37 CFR 1.821

I hereby state that the content of the paper and computer readable copies of the Sequence Listing, submitted in accordance with 37 CFR 1.821(c) and (e), respectively are the same.

Respectfully submitted,

KENING LI
ATTORNEY FOR APPLICANTS
REGISTRATION NO. 44,872
TELEPHONE: 302-992-3749
FACSIMILE: 302-892-1026

Dated: 04/10/2001

09740288



#5

SEQUENCE LISTING

<110> Allen, Stephen
Kinney, Anthony
Miao, Guo-Hua
Orozco, Emil

<120> PLANT BIOTIN SYNTHASE

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<140> US 09/740288

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<150> US 60/172929

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 Thr Arg Pro Glu Ile Gln Ala Ile Tyr Asp Ser Pro Leu Leu Asp Leu
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 Leu Phe His Gly Ala Gln Val His Arg Asn Val His Lys Phe Arg Glu
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 Val Gln Gln Cys Thr Leu Leu Ser Ile Lys Thr Gly Gly Cys Ser Glu
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 Asp Cys Ser Tyr Cys Pro Gln Ser Ser Arg Tyr Ser Thr Gly Leu Lys
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 35 40 45
 Gln Ala Val Tyr Asp Ser Pro Leu Leu Asp Leu Leu Phe His Gly Ala
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Arg	Ile	Thr	Met	Pro	Lys	Ala	Met	Val	Arg	Leu	Ser	Ala	Gly	Arg
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Val	Lys	Ser	Ile	Tyr	Asp	Ser	Pro	Ile	Leu	Asp	Leu	Leu	Phe	His	Gly
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Thr	Leu	Leu	Ser	Ile	Lys	Thr	Gly	Gly	Cys	Ser	Glu	Asp	Cys	Ser	Tyr
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Cys	Pro	Gln	Ser	Ser	Lys	Tyr	Asp	Thr	Gly	Val	Lys	Arg	Pro	Ser	Leu
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 <212> PRT
 <213> Hordeum vulgare

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 Ala Pro Phe Ser Ser Val Ser Ala Ala Ala Glu Ala Glu Arg Ala
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 Val Arg Asp Gly Pro Arg Asn Asp Trp Thr Arg Pro Glu Ile Gln Ala
 65 70 75 80
 Ile Tyr Asp Ser Pro Leu Leu Asp Leu Leu Phe His Gly Ala Gln Val
 85 90 95
 His Arg Asn Val His Lys Phe Arg Glu Val Gln Gln Cys Thr Leu Leu
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 Ser Ile Lys Thr Gly Gly Cys Ser Glu Asp Cys Ser Tyr Cys Pro Gln
 115 120 125

Ser Ser Arg Tyr Ser Thr Gly Leu Lys Ala Glu Lys Leu Met Lys Lys
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 Asp Ala Val Leu Glu Ala Lys Lys Ala Lys Glu Ala Gly Ser Thr
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 Arg Phe Cys Met Gly Ala Ala Trp Arg Glu Thr Ile Gly Arg Lys Thr
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 Met Glu Val Cys Cys Thr Leu Gly Met Leu Glu Lys Gln Gln Ala Glu
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 Glu Leu Lys Lys Ala Gly Leu Thr Ala Tyr Asn His Asn Leu Asp Thr
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 225 230 235 240
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 Ser Gly Gly Ile Ile Gly Leu Gly Glu Ala Glu Glu Asp Arg Val Gly
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 Pro Val Glu Ile Trp Glu Met Ile Arg Met Ile Ala Ser Ala Arg Ile
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 Ser Met Pro Glu Gln Ala Leu Cys Phe Leu Ala Gly Ala Asn Ser Ile
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 355 360 365
 Asp Gln Ala Met Phe Lys Ile Leu Gly Leu Ile Pro Lys Ala Pro Asn
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 cgcccgctgc tcctctatcc ctttctgct gctgotacta ccttaagcta tcaatatcat 180
 ggctctgatg ctgctagcgc gcaacctgcg ctcccgctc cgccccccgc tcgcgcgcgc 240
 cgccgcgttc tcgtcgccgc cgccggaggg ggagaggggc ctacgactca tgatgaacaa 300
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 gggagctgca tggagagaaa ccattggcag gaaatcaaac acactaggca tgatagagaa 540
 tgtcaaggaa ataagggtta tgggcattga ggtctgttgc acactaggca tgatagagaa 600
 acaacaagct gaagaactca agaaggctgg acttacagca tataatcata acctagata 660
 atcaagagag tattatccca acattattac cacaagatca tatgatgata gactgcagac 720

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<210> 20
 <211> 344
 <212> PRT
 <213> Zea mays

<400> 20
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 20 25 30
 Arg Ala Ile Arg Asp Gly Pro Arg Asn Asp Trp Ser Arg Pro Glu Ile
 35 40 45
 Gln Ala Val Tyr Asp Ser Pro Leu Leu Asp Leu Leu Phe His Gly Ala
 50 55 60
 Gln Ser Ser Arg Tyr Asn Thr Gly Leu Lys Ala Gln Lys Leu Met Asn
 65 70 75 80
 Lys Tyr Ala Val Leu Glu Ala Ala Lys Lys Ala Lys Glu Ser Gly Ser
 85 90 95
 Thr Arg Phe Cys Met Gly Ala Ala Trp Arg Glu Thr Ile Gly Arg Lys
 100 105 110
 Ser Asn Phe Asn Gln Ile Leu Glu Tyr Val Lys Glu Ile Arg Gly Met
 115 120 125
 Gly Met Glu Val Cys Cys Thr Leu Gly Met Ile Glu Lys Gln Gln Ala
 130 135 140
 Glu Glu Leu Lys Lys Ala Gly Leu Thr Ala Tyr Asn His Asn Leu Asp
 145 150 155 160
 Thr Ser Arg Glu Tyr Tyr Pro Asn Ile Ile Thr Thr Arg Ser Tyr Asp
 165 170 175
 Asp Arg Leu Gln Thr Leu Glu His Val Arg Glu Ala Gly Ile Ser Ile
 180 185 190
 Cys Ser Gly Gly Ile Ile Gly Leu Gly Glu Ala Glu Glu Asp Arg Val
 195 200 205
 Gly Leu Leu His Thr Leu Ala Thr Leu Pro Thr His Pro Glu Ser Val
 210 215 220
 Pro Ile Asn Ala Leu Val Ala Val Lys Gly Thr Pro Leu Glu Asp Gln
 225 230 235 240
 Lys Pro Val Glu Ile Trp Glu Met Ile Arg Met Ile Ala Thr Ala Arg
 245 250 255
 Ile Thr Met Pro Lys Ala Met Val Arg Leu Ser Ala Gly Arg Val Arg
 260 265 270
 Phe Ser Met Pro Glu Gln Ala Leu Cys Phe Leu Ala Gly Ala Asn Ser

275 280 285
 Ile Phe Ala Gly Glu Lys Leu Leu Thr Thr Ala Asn Asn Asp Phe Asp
 290 295 300
 Ala Asp Gln Ala Met Phe Lys Ile Leu Gly Leu Ile Pro Lys Ala Pro
 305 310 315 320
 Ser Phe Gly Glu Glu Glu Ala Ser Ala Ala Ala Pro Thr Glu Ser Glu
 325 330 335
 Arg Ser Glu Gln Ala Ala Ser Met
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<210> 21
 <211> 1515
 <212> DNA
 <213> Zea mays

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 gcaatgcaca cttctttcaa tcaagactgg ttgatgcagt gaagattgtt ctactgtccc 420
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 cttggaagca gcaaaaaagg caaaaagagtc tgggagcacc cgtttttgca tgggagctgc 540
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 aataaggggt atgggcatgg aggtctgttg cacactaggc atgatagaga aacaacaagc 660
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 gtattatccc aacattatta ccacaagatc atatgatgat agactgcaga ctcttgagca 780
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 ttgagactga atgggggata cccatgtcgc ctgatgtcaa aaaaaaaa aaataaaaaa 1440
 aaaaaaaa aaaaaaaa aaaaaaaa aaaaaaaa aaaaaaaa aaaaaaaa 1500
 aaaaaaaa aaaa 1515

<210> 22
 <211> 377
 <212> PRT
 <213> Zea mays

<400> 22
 Met Ala Leu Met Leu Leu Ala Arg Asn Leu Arg Ser Arg Leu Arg Pro
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 Pro Leu Ala Ala Ala Ala Phe Ser Ser Ala Ala Ala Glu Ala Glu
 20 25 30
 Arg Ala Ile Arg Asp Gly Pro Arg Asn Asp Trp Ser Arg Pro Glu Ile

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aacactggat	tgaaggccca	aaaattgatg	aacaaatag	ctgtcttgga	agcagcaaaa	480
aaggcaaaa	agtcctggag	caccctgttt	tgcatgggag	ctgcatggag	agaaacatt	540
ggcaggaat	caaaactcaa	ccagattott	gaatatgtca	aggaataaag	gggtatgggc	600
atggaggtct	gttgacact	agcatgata	gagaaacaac	aagctgaaga	actcaagaa	660
gctggactta	cagcatataa	tcataaccta	gatacatcaa	gagagtatta	tccaacatt	720
attaccacaa	gatcatatga	tgatagactg	cagactcttg	agcatgtccg	tgaagctgga	780
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gttgctgtaa	aaggcacacc	tcttgaggac	cagaagcctg	tagagatctg	ggaaatgatc	960
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gcggctccca	cagaatccga	gaggtctgat	caagctgctt	cgatgtagaa	tatatacata	1260
tcattaccga	ttatccgtat	cacggttggg	gcgaaactag	aactaccgtt	gtagctagag	1320
cattggattg	tagaaaccac	aacatttcac	tattttgtaa	ttgcttgaga	ctgaatgggg	1380
gatacccatg	tcgggctaga	tcaatggaca	acttccacac	aaaaaaaaaa	aaaaaaaaaa	1439

<210> 24
 <211> 377
 <212> PRT
 <213> Zea mays

<400> 24
 Met Ala Leu Met Leu Leu Ala Arg Asn Leu Arg Ser Arg Leu Arg Pro
 1 5 10 15
 Pro Leu Ala Ala Ala Ala Ala Phe Ser Ser Ala Ala Ala Glu Ala Glu
 20 25 30
 Arg Ala Ile Arg Asp Gly Pro Arg Asn Asp Trp Ser Arg Pro Glu Ile
 35 40 45
 Gln Ala Val Tyr Asp Ser Pro Leu Leu Asp Leu Leu Phe His Gly Ala
 50 55 60
 Gln Val His Arg Asn Val His Lys Phe Arg Glu Val Gln Gln Cys Thr
 65 70 75 80
 Leu Leu Ser Ile Lys Thr Gly Gly Cys Ser Glu Asp Cys Ser Tyr Cys
 85 90 95
 Pro Gln Ser Ser Arg Tyr Asn Thr Gly Leu Lys Ala Gln Lys Leu Met
 100 105 110
 Asn Lys Tyr Ala Val Leu Glu Ala Ala Lys Lys Ala Lys Glu Ser Gly
 115 120 125
 Ser Thr Arg Phe Cys Met Gly Ala Ala Trp Arg Glu Thr Ile Gly Arg
 130 135 140
 Lys Ser Asn Phe Asn Gln Ile Leu Glu Tyr Val Lys Glu Ile Arg Gly
 145 150 155 160
 Met Gly Met Glu Val Cys Cys Thr Leu Gly Met Ile Glu Lys Gln Gln
 165 170 175
 Ala Glu Glu Leu Lys Lys Ala Gly Leu Thr Ala Tyr Asn His Asn Leu
 180 185 190
 Asp Thr Ser Arg Glu Tyr Tyr Pro Asn Ile Ile Thr Thr Arg Ser Tyr
 195 200 205
 Asp Asp Arg Leu Gln Thr Leu Glu His Val Arg Glu Ala Gly Ile Ser
 210 215 220
 Ile Cys Ser Gly Gly Ile Ile Gly Leu Gly Glu Ala Glu Glu Asp Arg

<212> PRT
<213> Argemone mexicana

<400> 26

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Met Leu Lys Val Gln Ser Leu Arg Ala Arg Leu Arg Pro Leu Ile Phe
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20      25      30
Ala Val Gln Ala Glu Arg Thr Ile Lys Glu Gly Pro Arg Asn Asp Trp
35      40      45
Ser Arg Asp Glu Ile Lys Ser Val Tyr Asp Ser Pro Val Leu Asp Leu
50      55      60
Leu Phe His Ala Ala Gln Val His Arg His Ala His Asn Phe Arg Glu
65      70      75
Val Gln Gln Cys Thr Leu Leu Ser Val Lys Thr Gly Gly Cys Ser Glu
85      90      95
Asp Cys Ser Tyr Cys Pro Gln Ser Ser Arg Tyr Asp Thr Gly Val Lys
100     105     110
Ala Gln Lys Leu Met Asn Lys Asp Ala Val Leu Gln Ala Ala Glu Lys
115     120     125
Ala Lys Glu Ala Gly Ser Thr Arg Phe Cys Met Gly Ala Ala Trp Arg
130     135     140
Asp Thr Val Gly Arg Lys Thr Asn Phe Lys Gln Ile Leu Glu Tyr Val
145     150     155
Lys Glu Ile Arg Gly Met Gly Met Glu Val Cys Cys Thr Leu Gly Met
165     170     175
Ile Glu Lys Gln Gln Ala Val Glu Leu Lys Gln Ala Gly Leu Thr Ala
180     185     190
Tyr Asn His Asn Leu Asp Thr Ser Arg Glu Tyr Tyr Pro Asn Ile Ile
195     200     205
Thr Thr Arg Ser Tyr Asp Glu Arg Leu Glu Thr Leu Gln Phe Val Arg
210     215     220
Glu Ala Gly Ile Asn Val Cys Ser Gly Gly Ile Ile Gly Leu Gly Glu
225     230     235
Ala Glu Glu Asp Arg Val Gly Leu Leu His Thr Leu Ala Thr Leu Pro
245     250     255
Ser His Pro Glu Ser Val Pro Ile Asn Ala Leu Leu Ala Val Lys Gly
260     265     270
Thr Pro Leu Glu Asp Gln Lys Pro Val Glu Ile Trp Glu Met Ile Arg
275     280     285
Met Ile Ala Thr Ala Arg Ile Val Met Pro Lys Ala Met Val Arg Leu
290     295     300
Ser Ala Gly Arg Val Arg Phe Ser Met Ser Glu Gln Ala Leu Cys Phe
305     310     315
Leu Ala Gly Ala Asn Ser Ile Phe Thr Gly Glu Lys Leu Leu Thr Thr
325     330     335
Pro Asn Asn Asp Phe Asp Ala Asp Gln Met Met Phe Lys Ile Leu Gly
340     345     350
Leu Thr Pro Lys Ala Pro Asn Phe Asp Gln Thr Ser Thr Ser Phe Glu
355     360     365
Ala Glu Arg Cys Glu Gln Glu Ala Thr Ala Ser
370     375

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<210> 27
<211> 1526



<212> DNA
<213> Glycine max

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gttcacagac atgtctcataa ctccaggga gttcagcagt gtactcttct gtctatcaaa 480
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gcaactgcac gtatcgtaat gccaaaagca atggctcagg ttatcagctg cagagtttga 1140
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aatctcagct ttgaagacac aaactccaac acttaaaaat aaatattgaa attattgatt 1500
ttccctaaaa aaaaaaaaaa aaaaaa 1526

<210> 28
<211> 415
<212> PRT
<213> Glycine max

<400> 28
Thr Lys Pro Asn Pro Lys His Lys Tyr Arg Cys Cys Leu Leu Ser Leu
1 5 10 15
Ser Cys Leu Tyr Ser Gln Ile Ser His Ser Phe Ser Val Val Ser Leu
20 25 30
Pro Asn Phe Glu Phe Glu Ser Lys Asn Met Phe Leu Ala Arg Pro Ile
35 40 45
Phe Arg Ala Pro Ser Leu Trp Ala Leu His Ser Ser Tyr Ala Tyr Ser
50 55 60
Ser Ala Ser Ala Ala Ala Ile Gln Ala Glu Arg Ala Ile Lys Glu Gly
65 70 75 80
Pro Arg Asn Asp Trp Ser Arg Asp Gln Val Lys Ser Ile Tyr Asp Ser
85 90 95
Pro Ile Leu Asp Ser Leu Phe His Gly Ala Gln Val His Arg His Ala
100 105 110
His Asn Phe Arg Glu Val Gln Gln Cys Thr Leu Leu Ser Ile Lys Thr
115 120 125
Gly Gly Cys Ser Glu Asp Cys Ser Tyr Cys Pro Gln Ser Ser Lys Tyr
130 135 140


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tccggaatca tttcctgtga acatgttagt ggctatcaaa ggaacaccac tggaaaggaaa 960
caagaaggtg gaatttgaga atatgttgag aatggttgag acggctagaa tcgtcatgcc 1020
taaaaccatc gtgcgttttg cagctggaag aggagaattg acgcgaggaac aacaggtcctt 1080
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cgttggaagg ggtgtcgatt ccgtcgtttt caacagatgg ggattaaagc ccatggaaaag 1200
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<210> 30
<211> 417
<212> PRT
<213> Glycine max

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Ser Asn Thr Pro Lys Leu Ala Pro Ile Ser Ser Ser Val Arg Leu Gln
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Val Gln Lys Ser Arg Asn Tyr Gly Thr Val Ser Ser Val Pro Pro Gln
35 40 45
Ala Thr Glu Thr Ser Ser Thr Ser Pro Ser Lys Asp Val Tyr Gln Glu
50 55 60
Ala Leu Asn Ala Thr Glu Pro Arg Ser Asn Trp Thr Arg Glu Glu Ile
65 70 75 80
Lys Ala Ile Tyr Asp Lys Pro Leu Met Glu Leu Cys Trp Gly Ala Gly
85 90 95
Ser Leu His Arg Lys Phe His Ile Pro Gly Ala Ile Gln Met Cys Thr
100 105 110
Leu Leu Asn Ile Lys Thr Gly Gly Cys Ser Glu Asp Cys Ser Tyr Cys
115 120 125
Ala Gln Ser Ser Arg Tyr Gln Thr Gly Leu Lys Ala Ser Lys Met Val
130 135 140
Ser Val Glu Ser Val Leu Ala Ala Ala Arg Ile Ala Lys Asp Asn Gly
145 150 155 160
Ser Thr Arg Phe Cys Met Gly Ala Ala Trp Arg Asp Met Arg Gly Arg
165 170 175
Lys Thr Asn Leu Lys Asn Val Lys Thr Met Val Ser Glu Ile Arg Gly
180 185 190
Met Gly Met Glu Val Cys Val Thr Leu Gly Met Ile Asp Ala Glu Gln
195 200 205
Ala Gln Glu Leu Lys Glu Ala Gly Leu Thr Ala Tyr Asn His Asn Val
210 215 220
Asp Thr Ser Arg Asp Phe Tyr Pro Lys Val Ile Thr Thr Arg Thr Tyr
225 230 235 240
Asp Glu Arg Leu Asp Thr Ile Lys Asn Val Arg Glu Ala Gly Ile Asn
245 250 255
Val Cys Thr Gly Gly Ile Leu Gly Leu Gly Glu Asn Lys Ser Asp His
260 265 270

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Ile Gly Leu Leu Glu Thr Val Ala Thr Leu Pro Ser His Pro Glu Ser
 275 280 285
 Phe Pro Val Asn Met Leu Val Ala Ile Lys Gly Thr Pro Leu Glu Gly
 290 295 300
 Asn Lys Lys Val Glu Phe Glu Asn Met Leu Arg Met Val Ala Thr Ala
 305 310 315 320
 Arg Ile Val Met Pro Lys Thr Ile Val Arg Leu Ala Ala Gly Arg Gly
 325 330 335
 Glu Leu Ser Glu Glu Gln Gln Val Leu Cys Phe Met Ala Gly Ala Asn
 340 345 350
 Ala Val Phe Thr Gly Glu Thr Met Leu Thr Thr Pro Ala Val Gly Trp
 355 360 365
 Gly Val Asp Ser Val Val Phe Asn Arg Trp Gly Leu Arg Pro Met Glu
 370 375 380
 Ser Phe Glu Val Glu Ala Leu Lys Asn Asp Lys Pro Ala Thr Thr Asn
 385 390 395 400
 Thr Glu Ile Pro Val Glu Ala Ser Lys Ala Glu Met Pro Gly Thr Val
 405 410 415
 Ala

<210> 31
 <211> 1032
 <212> DNA
 <213> Triticum aestivum

<400> 31
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 ttgaatatgt caaggacata agaggtatgg gcatggaggt ctgttgcacc ctgggcatgc 180
 tagagaaaca acaagctgaa gaactcaaga aggctggact tacagcttat aatcataacc 240
 tagatacatc aagagaatat taccccaaca ttatttctac aagatcgtag gatgatagat 300
 tacagactct tcagcatgtc cgtgaagctg gaataagcgt ctgctcaggt ggaattattg 360
 gtcttggaga ggccgaggaa gaccgtgtag ggctgttgc aactgtgcc aactttgccaa 420
 cacacccaga gagcgttccat atcaatgcat tgattgtctg caaaggcagc cctcttcagg 480
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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1020
 aaaaaaaaaa aa 1032

<210> 32
 <211> 263
 <212> PRT
 <213> Triticum aestivum

<400> 32
 Thr Arg Asp Ala Val Leu Glu Ala Ala Lys Lys Ala Lys Glu Ala Gly
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Ser Thr Arg Phe Cys Met Gly Ala Ala Trp Arg Glu Thr Ile Gly Arg
 20 25 30
 Lys Thr Asn Phe Asn Gln Ile Leu Glu Tyr Val Lys Asp Ile Arg Gly
 35 40 45
 Met Gly Met Glu Val Cys Cys Thr Leu Gly Met Leu Glu Lys Gln Gln
 50 55 60
 Ala Glu Glu Leu Lys Lys Ala Gly Leu Thr Ala Tyr Asn His Asn Leu
 65 70 75 80
 Asp Thr Ser Arg Glu Tyr Tyr Pro Asn Ile Ile Ser Thr Arg Ser Tyr
 85 90 95
 Asp Asp Arg Leu Gln Thr Leu Gln His Val Arg Glu Ala Gly Ile Ser
 100 105 110
 Val Cys Ser Gly Gly Ile Ile Gly Leu Gly Glu Ala Glu Glu Asp Arg
 115 120 125
 Val Gly Leu Leu His Thr Leu Ala Thr Leu Pro Thr His Pro Glu Ser
 130 135 140
 Val Pro Ile Asn Ala Leu Ile Ala Val Lys Gly Thr Pro Leu Gln Asp
 145 150 155 160
 Gln Lys Pro Val Glu Ile Trp Glu Met Ile Arg Met Ile Ala Ser Ala
 165 170 175
 Arg Ile Val Met Pro Lys Ala Met Val Arg Leu Ser Ala Gly Arg Val
 180 185 190
 Arg Phe Ser Met Pro Glu Gln Ala Leu Cys Phe Leu Ala Gly Ala Asn
 195 200 205
 Ser Ile Phe Ala Gly Glu Lys Leu Leu Thr Thr Ala Asn Asn Asp Phe
 210 215 220
 Asp Ala Asp Gln Ala Met Phe Lys Ile Leu Gly Leu Ile Pro Lys Ala
 225 230 235 240
 Pro Asn Phe Gly Asp Glu Glu Val Met Val Ala Ala Pro Thr Glu Arg
 245 250 255
 Cys Glu Gln Ala Ala Leu Met
 260

<210> 33
 <211> 378
 <212> PRT
 <213> Arabidopsis thaliana

<400> 33
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 20 25 30
 Ser Ala Glu Ala Glu Arg Thr Ile Arg Glu Gly Pro Arg Asn Asp Trp
 35 40 45
 Ser Arg Asp Glu Ile Lys Ser Val Tyr Asp Ser Pro Leu Leu Asp Leu
 50 55 60
 Leu Phe His Gly Ala Gln Val His Arg His Val His Asn Phe Arg Glu
 65 70 75 80
 Val Gln Gln Cys Thr Leu Leu Ser Ile Lys Thr Gly Gly Cys Ser Glu
 85 90 95
 Asp Cys Ser Tyr Cys Pro Gln Ser Ser Arg Tyr Ser Thr Gly Val Lys
 100 105 110
 Ala Gln Arg Leu Met Ser Lys Asp Ala Val Ile Asp Ala Ala Lys Lys
 115 120 125

Ala Lys Glu Ala Gly Ser Thr Arg Phe Cys Met Gly Ala Ala Trp Arg
 130 135 140
 Asp Thr Ile Gly Arg Lys Thr Asn Phe Ser Gln Ile Leu Glu Tyr Ile
 145 150 155 160
 Lys Glu Ile Arg Gly Met Gly Met Glu Val Cys Cys Thr Leu Gly Met
 165 170 175
 Ile Glu Lys Gln Gln Ala Leu Glu Leu Lys Lys Ala Gly Leu Thr Ala
 180 185 190
 Tyr Asn His Asn Leu Asp Thr Ser Arg Glu Tyr Tyr Pro Asn Val Ile
 195 200 205
 Thr Thr Arg Ser Tyr Asp Asp Arg Leu Glu Thr Leu Ser His Val Arg
 210 215 220
 Asp Ala Gly Ile Asn Val Cys Ser Gly Gly Ile Ile Gly Leu Gly Glu
 225 230 235 240
 Ala Glu Glu Asp Arg Ile Gly Leu Leu His Thr Leu Ala Thr Leu Pro
 245 250 255
 Ser His Pro Glu Ser Val Pro Ile Asn Ala Leu Leu Ala Val Lys Gly
 260 265 270
 Thr Pro Leu Glu Asp Gln Lys Pro Val Glu Ile Trp Glu Met Ile Arg
 275 280 285
 Met Ile Gly Thr Ala Arg Ile Val Met Pro Lys Ala Met Val Arg Leu
 290 295 300
 Ser Ala Gly Arg Val Arg Phe Ser Met Ser Glu Gln Ala Leu Cys Phe
 305 310 315 320
 Leu Ala Gly Ala Asn Ser Ile Phe Thr Gly Glu Lys Leu Leu Thr Thr
 325 330 335
 Pro Asn Asn Asp Phe Asp Ala Asp Gln Leu Met Phe Lys Thr Leu Gly
 340 345 350
 Leu Ile Pro Lys Pro Pro Ser Phe Ser Glu Asp Asp Ser Glu Ser Glu
 355 360 365
 Asn Cys Glu Lys Val Ala Ser Ala Ser His
 370 375

<210> 34

<211> 362

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 34

Met Phe Thr Arg Thr Ile Arg Gln Gln Ile Arg Arg Phe Phe Ala Leu
 1 5 10 15
 Phe Leu Val Arg Asn Asn Trp Thr Arg Glu Glu Ile Gln Lys Ile Tyr
 20 25 30
 Asp Thr Pro Leu Ile Asp Leu Ile Phe Arg Ala Ala Ser Ile His Arg
 35 40 45
 Lys Phe His Asp Pro Lys Lys Val Gln Gln Cys Thr Leu Ser Ile
 50 55 60
 Lys Thr Gly Gly Cys Thr Glu Asp Cys Lys Tyr Cys Ala Gln Ser Ser
 65 70 75 80
 Arg Tyr Asn Thr Gly Val Lys Ala Thr Lys Leu Met Lys Ile Asp Glu
 85 90 95
 Val Leu Glu Lys Ala Lys Ile Ala Lys Ala Lys Gly Ser Thr Arg Phe
 100 105 110
 Cys Met Gly Ser Ala Trp Arg Asp Leu Asn Gly Arg Asn Arg Thr Phe
 115 120 125

Lys Asn Ile Leu Glu Ile Ile Lys Glu Val Arg Ser Met Asp Met Glu
 130 135 140
 Val Cys Val Thr Leu Gly Met Leu Asn Glu Gln Gln Ala Lys Glu Leu
 145 150 155 160
 Lys Asp Ala Gly Leu Thr Ala Tyr Asn His Asn Leu Asp Thr Ser Arg
 165 170 175
 Glu Tyr Tyr Ser Lys Ile Ile Ser Thr Arg Thr Tyr Asp Glu Arg Leu
 180 185 190
 Asn Thr Ile Asp Asn Leu Arg Lys Ala Gly Leu Lys Val Cys Ser Gly
 195 200 205
 Gly Ile Leu Gly Leu Gly Glu Lys Lys His Asp Arg Val Gly Leu Ile
 210 215 220
 His Ser Leu Ala Thr Met Pro Thr His Pro Glu Ser Val Pro Phe Asn
 225 230 235 240
 Leu Leu Val Pro Ile Pro Gly Thr Pro Val Gly Asp Ala Val Lys Glu
 245 250 255
 Arg Leu Pro Ile His Pro Phe Leu Arg Ser Ile Ala Thr Ala Arg Ile
 260 265 270
 Cys Met Pro Lys Thr Ile Ile Arg Phe Ala Ala Gly Arg Asn Thr Cys
 275 280 285
 Ser Glu Ser Glu Gln Ala Leu Ala Phe Met Ala Gly Ala Asn Ala Val
 290 295 300
 Phe Thr Gly Glu Lys Met Leu Leu Leu Leu Phe Leu Asp Ser Asp
 305 310 315 320
 Ser Gln Leu Phe Tyr Asn Trp Gly Leu Glu Gly Met Gln Ser Phe Glu
 325 330 335
 Tyr Gly Thr Ser Thr Glu Gly Glu Asp Gly Thr Phe Thr Leu Pro Pro
 340 345 350
 Lys Glu Arg Leu Ala Pro Ser Pro Ser Leu
 355 360

<210> 35

<211> 363

<212> PRT

<213> Schizosaccharomyces pombe

<400> 35

Met Phe Thr Arg Thr Ile Arg Gln Gln Ile Arg Arg Ser Ser Ala Leu
 1 5 10 15
 Ser Leu Val Arg Asn Asn Trp Thr Arg Glu Ile Gln Lys Ile Tyr
 20 25 30
 Asp Thr Pro Leu Ile Asp Leu Ile Phe Arg Ala Ala Ser Ile His Arg
 35 40 45
 Lys Phe His Asp Pro Lys Lys Val Gln Gln Cys Thr Leu Ser Ile
 50 55 60
 Lys Thr Gly Gly Cys Thr Glu Asp Cys Lys Tyr Cys Ala Gln Ser Ser
 65 70 75 80
 Arg Tyr Asn Thr Gly Val Lys Ala Thr Lys Leu Met Lys Ile Asp Glu
 85 90 95
 Val Leu Glu Lys Ala Lys Ile Ala Lys Ala Lys Gly Ser Thr Arg Phe
 100 105 110
 Cys Met Gly Ser Ala Trp Arg Asp Leu Asn Gly Arg Asn Arg Thr Phe
 115 120 125
 Lys Asn Ile Leu Glu Ile Ile Lys Glu Val Arg Ser Met Asp Met Glu
 130 135 140

Val Cys Val Thr Leu Gly Met Leu Asn Glu Gln Gln Ala Lys Glu Leu
 145 150 155 160
 Lys Asp Ala Gly Leu Thr Ala Tyr Asn His Asn Leu Asp Thr Ser Arg
 165 170 175
 Glu Tyr Tyr Ser Lys Ile Ile Ser Thr Arg Thr Tyr Asp Glu Arg Leu
 180 185 190
 Asn Thr Ile Asp Asn Leu Arg Lys Ala Gly Leu Lys Val Cys Ser Gly
 195 200 205
 Gly Ile Leu Gly Leu Gly Glu Lys Lys His Asp Arg Val Gly Leu Ile
 210 215 220
 His Ser Leu Ala Thr Met Pro Thr His Pro Glu Ser Val Pro Phe Asn
 225 230 235 240
 Leu Leu Val Pro Ile Pro Gly Thr Pro Val Gly Asp Ala Val Lys Glu
 245 250 255
 Arg Leu Pro Ile His Pro Phe Leu Arg Ser Ile Ala Thr Ala Arg Ile
 260 265 270
 Cys Met Pro Lys Thr Ile Ile Arg Phe Ala Ala Gly Arg Asn Thr Cys
 275 280 285
 Ser Glu Ser Glu Gln Ala Leu Ala Phe Met Ala Gly Ala Asn Ala Val
 290 295 300
 Phe Thr Gly Glu Lys Met Leu Thr Thr Pro Ala Val Ser Trp Asp Ser
 305 310 315 320
 Asp Ser Gln Leu Phe Tyr Asn Trp Gly Leu Glu Gly Met Gln Ser Phe
 325 330 335
 Glu Tyr Gly Thr Ser Thr Glu Gly Glu Asp Gly Thr Phe Thr Leu Pro
 340 345 350
 Pro Lys Glu Arg Leu Ala Pro Ser Pro Ser Leu
 355 360

<210> 36
 <211> 12
 <212> FRT
 <213> biotin synthase conserved sequence element

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 <222> (2)..(2)
 <223> Xaa represents any amino acid

<220>
 <221> UNSURE
 <222> (4)..(4)
 <223> Xaa represents any amino acid

<220>
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 <223> Xaa represents any amino acid

<220>
 <221> UNSURE
 <222> (11)..(11)



223> Xaa represents any amino acid

<400> 36

Gly Xaa Cys Xaa Glu Asp Cys Xaa Tyr Cys Xaa Gln

1

5

10

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